ATGTTCGGCTCCGCCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG

TTGTGGAAGCTCGCGGGGTTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC

ACCCTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG

GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC

CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACTCAAG

CTGGTCCATGTTGCTGGTCCTGGCCCCACAGGGCCCATCAAGATTTTCCCCTTCAAATCC

CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC

TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC

TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC

TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT

TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT

GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC

TCAGGGGCTGCTCTGGGGGTCCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC

CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTTGGCATACAACCTGCTGGAAGGACAC

CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC

CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCCAGTACTTGTCACCCCGGGCC

AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCACTGACAGATTTTCAG

ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCCACCTTTGCCCTGGCCAGTGGGGAGT

ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTTGTG

ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT

GAACCCAGTGATACGGACCCGGAGCCCCGAACTCTGAACCCCTCTCCGGCTGGATGGTTC

GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCCTCTGCCGGCCACCCCCACT

Figure 1A

ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT

TCACCCCCGCAGGAGGAAGCCAGAGGCCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG

GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG

GGGGAGATGGTGGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC

CAGAAGGAAGTGGAAGCGGAACTCTGTCGCCCCTTGTTGGTGTGTCCCCTGGAGGGGCCT

GAGGGCATACGGGGCAGGGAATGCTTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG

GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG

ATAGAGCCGGAGGCCCAGGCCCAGAGGTCGCCCAGGCCCACGGGCTCAGATCTGCTCCCT

GGAGCCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC

TATTTGGTGCTGGAGCCTGATGCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC

CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA

TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC

AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGGGAGCGGAAACAGGGAGAGCAGT

CTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACC

TTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGTGACCATGGTAGTTGGA

GCCTCAGTCCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGACCACCGACTCCGGCTCT

TCCTGGATGTTGAGGTGTTCAGCGATGCCCAGGAGGAGTTCCAGTGCTGCCTCAAGGTGC

CAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTGGTTGTGTCTGACCGCA

GGCTGTACCTGTTGA

Figure 1B.

ATGTTCGGCTCCGCCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG

TTGTGGAAGCTCGCGGGGTTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC

ACCCTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG

GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC

CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACTCAAG

CTGGTCCATGTTGCTGGTCCTGGCCCCACAGGGCCCATCAAGATTTTCCCCTTCAAATCC

CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC

TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC

TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC

TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT

TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT

GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC

TCAGGGGCTGCTCTGGGGGTCCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC

CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTTGGCATACAACCTGCTGGAAGGACAC

CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC

CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCCAGTACTTGTCACCCCGGGCC

AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCACTGACAGATTTTCAG

ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCCACCTTTGCCCTGGCCAGTGGGGAGT

ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTTGTG

ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT

GAACCCAGTGATACGGACCCGGAGCCCCGAACTCTGAACCCCTCTCCGGCTGGATGGTTC

GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

Figure 2A

TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCCTCTGCCGGCCACCCCCACT

ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT

TCACCCCCGCAGGAGGAAGCCAGAGGCCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG

GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG

GGGGAGATGGTGGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC

CAGAAGGAAGTGGAAGCGGAACTCTGTCGCCCCTTGTTGGTGTGTCCCCTGGAGGGGCCT

GAGGGCGTACGGGGCAGGGAATGCTTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG

GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG

ATAGAGCCGGAGGCCCAGGCCCAGAGGTCGCCCAGGCCCACGGGCTCAGATCTGCTCCCT

GGAGCCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC

TATTTGGTGCTGGAGCCTGATGCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC

CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA

TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC

AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGTGTGTCCTAAC

TGTGGTAGTGACCACGTGGTTCTCCTCGCTGTGTCTCGGGGAACCCCCAACAGGGAGCGG

AAACAGGGAGAGCAGTCTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCT

GGCCATGGTGACCACCTTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGT

GACCATGGTAGTTGGAGCCTCAGTCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGAC

CACCGACTCCGGCTCTTCCTGGATGTTGAGGTGTTCAGCGATGCCCAGGAGGAGTTCCAG

TGCTGCCTCAAGGTGCCAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTG

GTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGGAGATGCGTGAGCCTCCA

GCTAGCTGGCTGCAGCTGACCCTGGCTGTTCCCCTGCAGGATCTGAGTGGCATAGAGCTG

Figure 2B

GGCCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGCAGCTGGGGCGGGCCGCTGTGTGCTG

CTGCCCCGAGATGCCAGGCATTGCCGGGCCTTCCTAGAGGAGCTCCTTGATGTCTTGCAG

TCTCTGCCCCCTGCCTGGAGGAACTGTGTCAGTGCCACAGAGGAGGAGGTCACCCCCCAG

CACCGGCTCTGGCCATTGCTGGAAAAAGACTCATCCTTGGAGGCTCGCCAGTTCTTCTAC

CTTCGGGCGTTCCTGGTTGAAGGCCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCG

TCCACCCTGTTCCTGTTAGATGAGGATGCTGCAGGGTCCCCGGCAGAGCCCTCTCCTCCA

GCAGCATCTGGCGAAGCCTCTGAGAAGGTGCCTCCCTCGGGGCCGGGCCCTGCTGTGCGT

GTCAGGGAGCAGCAGCCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCCT

GAGGACTTGCGGCTGCTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTC

CGTGTGGTGTGTCAGGAGCAGCTGACAGCCCTGCTTGCCTGGATCCGGGAACCATGGGAG

GAGCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA

Figure 2C.

MFGSAPQRPVAMTTAQRDSLLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHL

GPWGPGQTGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGPTGPIKIFPFKS

LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN

FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGP

SGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN

PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQTHTSLGLSPMGPPLPWPVGS

TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTDPEPRTLNPSPAGWF

VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP

SPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEAGEEEEEEQD

QKEVEAELCRPLLVCPLEGPEGIRGRECFLRVTSAHLFEVELQAARTLERLELQSLEAAE

IEPEAQAQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDAHAAVQELLAVLT

PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTGSGNRESS

LWLLLRLPALSATLLAMVTTLTGPRTAHLRHRAPVTMVVGASVPPLSAVASALWTTDSGS

SWMLRCSAMPRRSSSAASRCQWHWQATLGSSCALWLCLTAGCTC

Figure 3.

MFGSAPQRPVAMTTAQRDSLLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHL

GPWGPGQTGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGPTGPIKIFPFKS

LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN

FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGP

SGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN

PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQTHTSLGLSPMGPPLPWPVGS

TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTDPEPRTLNPSPAGWF

VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP

SPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEAGEEEEEEQD

QKEVEAELCRPLLVCPLEGPEGVRGRECFLRVTSAHLFEVELQAARTLERLELQSLEAAE

IEPEAQAQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDAHAAVQELLAVLT

PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTESPAVCPN

CGSDHVVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRAKNSPPQAPSTR

DHGSWSLSPPPERCGLRSVDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLV

VVSDRRLYLLKVTGEMREPPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGAGRCVL

LPRDARHCRAFLEELLDVLQSLPPAWRNCVSATEEEVTPQHRLWPLLEKDSSLEARQFFY

LRAFLVEGPSTCLVSLLLTPSTLFLLDEDAAGSPAEPSPPAASGEASEKVPPSGPGPAVR

VREQQPLSSLSSVLLYRSAPEDLRLLFYDEVSRLESFWALRVVCQEQLTALLAWIREPWE

ELFSIGLRTVIQEALALDR

Figure 4.

```
>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
           (AF082516) I-1 receptor candidate protein [Homo sapiens]
           Length = 1504

 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLSLKLVHVAGP-GPTG---------PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
           +L  T  LK + V+G  GP G         P  +  FKSL  +E+       + GL
Sbjct: 180 ILDFTCRLKYLKVSGTEGPFGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157 SQLETLICSRSLQALEELL--------------SACGGDFCSALP-WLALLSANFSYNXX 201
             L TL    S  +++E+L               +   G   + +P W AL + + S+N
Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299

Query: 202 XXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
                           HN +      L  L  L HLD+SYN+L  +  +       +
Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

Query: 262 VLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
            L L GN L SL GL +L +L +LDL  N +E   E+  +  L  L  + L  NPL   P
Sbjct: 359 TLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418

Query: 322 EHRAATAQYLSPRARD 337
           ++R         RA +
Sbjct: 419 DYRTKVLAQFGERASE 434
```

Figure 5.

```
101 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 2150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1644 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 1693

2151 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAG..................  2183
     |||||||||||||||||||||||||||||||
1694 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGT 1743

2184 .........ACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 2224
             ||||||||||||||||||||||||||||||||||||||||||||
1794 GAACCCCCAACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 1843

2225 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 2274
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1844 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 1893

2825 TCATCCTTGGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2874
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2444 TCATCCTTGGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2493

3375 ATCTGGGCCCCTCCATGACCTTCCACACTGGATGCCTCTTTCCCTGCAGG 3424
                                                    |||
2494 ..............................................AGG 2496

3425 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 3474
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2497 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 2546
```

Figure 6.

```
Query= sequence
         (1114 letters)

Database: newnr
           228,478 sequences; 162,186,938 total letters

Searching.....................................................done

                                                                    Score     E
Sequences producing significant alignments:                         (bits)  Value

gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melano...   127  5e-28
gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC3310...    68  4e-10
gb|AAF57514.1| (AE003794) CG8595 gene product [Drosophila melano...    47  0.001

>gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melanogaster]
           Length = 1289

 Score =  127 bits (317), Expect = 5e-28
 Identities = 99/321 (30%), Positives = 149/321 (45%), Gaps = 11/321 (3%)

Query: 38  KLAGLLRESGDVVXXXXXXXXXXXXXXXXXNHVF------ELHLGPWGPGQTGFVALPSH 91
           +LA LLR++GD +                  N  F      E+  G        F  +
Sbjct: 8   ELANLLRQNGDKILSSEFTLTLSGSLLRALNDSFTLIADTEIGTGAGYLQPQSFQVVKPI 67

Query: 92  PADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP-TGPIKIFPFKSLRHLELRGVPLHCLH 150
            A S V   LQ + D +QKT  LKL +         G I I  F++LR LE+  + +  +
Sbjct: 68  NAKSSVFPDLQLVHDFVQKTTLLKLTYFPSEHYFEGAIDIAKFRALRRLEVNKINIGQVV 127

Query: 151 GLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSANFSYNXXXXXXXXXXX 210
           G++ +  QL+ LIC +SL +++++++ CGGD  +   W  L +A+FSYN
Sbjct: 128 GIQPLRGQLQHLICVKSLTSVDDIITRCGGDNSNGFVWNELKTADFSYNSLRSVDTALEF 187

Query: 211 XXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGA-ALGVLILRGNE 269
                     HN++      +  L  L  LD+SYN L  +P+        L +L +  N
Sbjct: 188 AQHLQHLNLRHNKLTSVAA-IKWLPHLKTLDLSYNCLTHLPQFHMEACKRLQLLNISNNY 246

Query: 270 LRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHPEHRAATAQ 329
           +  L  + +L  L +LDL+ N L  H +L PL  L  L L L+GNPL  +P+HR ATAQ
Sbjct: 247 VEELLDVAKLDALYNLDLSDNCLLEHSQLLPLSALMSLIVLNLQGNPLACNPKHRQATAQ 306

Query: 330 YLSPRARDAATGFLLDGKVLS 350
           YL      A   F+LD + L+
Sbjct: 307 YL--HKNSATVKFVLDFEPLT 325
```

Figure 7A

```
 Score = 41.4 bits (95), Expect = 0.054
 Identities = 41/151 (27%), Positives = 62/151 (40%), Gaps = 20/151 (13%)

Query: 814  VDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLLKVTGEMRE 873
            +DHRL+L+     F +  E F+    K  +           LVV+S+ + YL++   E  +
Sbjct: 1018 IDHRLKLYFYQRKFKEDGEHFKWLAKGRIYNEQTQSLGEGLVVMSNCKCYLMEAFAEPHD 1077

Query: 874  PPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGA-------GRCVLLPRDARHCRAF 926
              A WL+  ++V +  L  I+L        L W  G         G  VLL  D
Sbjct: 1078 DVAKWLRQVVSVAVNRLVAIDL--------LPWKLGLSFTLKDWGGFVLLLHDMLR---- 1125

Query: 927  LEELLDVLQSLPPAWRNCVSATEEEVTPQHR 957
              E LL+ LQ +P      C     +  VT  H+
Sbjct: 1126 TESLLNYLQQIPLP-EQCKLNHQPSVTLSHQ 1155


>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
           (AF082516) I-1 receptor candidate protein [Homo sapiens]
           Length = 1504

 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLSLKLVHVAGP-GPTG---------PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
            +L  T  LK + V+G  GP G         P  +  FKSL  +E+        + GL
Sbjct: 180 ILDFTCRLKYLKVSGTEGPFGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157 SQLETLICSRSLQALEELL--------------SACGGDFCSALP-WLALLSANFSYNXX 201
              L TL    S  +++E+L                +   G   + +P W AL + + S+N
Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299

Query: 202 XXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
                             HN +      L  L  L HLD+SYN+L  +  +       +
Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

Query: 262 VLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
             L L GN L SL GL +L +L +LDL  N +E   E+  +  L  L  + L  NPL   P
Sbjct: 359 TLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418

Query: 322 EHRAATAQYLSPRARD 337
            ++R          RA +
Sbjct: 419 DYRTKVLAQFGERASE 434
```

Figure 7B

```
FL1-18_SPLICE_VARIANT              ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD-----------
FL1-18                             ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD-----------
Drosophila_melanogaster_CG9044     ------MDPQK--------------ITELANLLRQNGD-----------
imidazoline_receptor_candidate     MATARTFGPEREAEPAKEARVVGSELVDTYTVYIIQVTDGSHEWTVKHRY
                                          *::         .      :   :  : :  *

FL1-18_SPLICE_VARIANT              ---------VVLSGCSTLSLLTP--------------------------
FL1-18                             ---------VVLSGCSTLSLLTP--------------------------
Drosophila_melanogaster_CG9044     ---------KILSSEFTLTLSGS--------------------------
imidazoline_receptor_candidate     SDFHDLHEKLVAERKIDKNLLPPKKIIGKNSRSLVEKREKDLEVYLQKLL
                                             : .     .*  .

FL1-18_SPLICE_VARIANT              ------TLQQLNHVFELHLG--------------------------PWG
FL1-18                             ------TLQQLNHVFELHLG--------------------------PWG
Drosophila_melanogaster_CG9044     ------LLRALNDSFTLIADT-------------------------EIG
imidazoline_receptor_candidate     AAFPGVTPRVLAHFLHFHFYEINGITAALAEELFEKGEQLLGAGEVFAIG
                                           : * . : :                                *

FL1-18_SPLICE_VARIANT              PG----Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
FL1-18                             PG----Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
Drosophila_melanogaster_CG9044     TGAGYLQPQSFQVVKPINAKSSVFPDLQLVHDFVQKTTLLKLTYFPSEHY
imidazoline_receptor_candidate     PLQLYAVTEQLQQGKPTCASGDAKTDLGHILDFTCRLKYLKVSGTEGPFG
                                   .         :    .  *.. .  :*  : *.  :   **:    .

FL1-18_SPLICE_VARIANT              -------TGPIKIFPFKSLRHLELRGVPLHCLHGLRGIYSQLETLICSRS
FL1-18                             -------TGPIKIFPFKSLRHLELRGVPLHCLHGLRGIYSQLETLICSRS
Drosophila_melanogaster_CG9044     F------EGAIDIAKFRALRRLEVNKINIGQVVGIQPLRGQLQHLICVKS
imidazoline_receptor_candidate     TSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASKPTLATLSVRFS
                                           .:.:  *::*:::*:       : *:      *  *    *

FL1-18_SPLICE_VARIANT              LQALEELLSACGGDFCSALP--------------WLALLSANFSYNALT
FL1-18                             LQALEELLSACGGDFCSALP--------------WLALLSANFSYNALT
Drosophila_melanogaster_CG9044     LTSVDDIITRCGGDNSNGFV--------------WNELKTADFSYNSLR
imidazoline_receptor_candidate     ATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSIS
                                     ::.:::   ..:  .                  *  * : ::*:*::

FL1-18_SPLICE_VARIANT              ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
FL1-18                             ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
Drosophila_melanogaster_CG9044     SVDTALEFAQHLQHLNLRHNKLTSVA-AIKWLPHLKTLDLSYNCLTHLPQ
imidazoline_receptor_candidate     EIDESVKLIPKIEFLDLSHNGLLVVD-NLQHLYNLVHLDLSYNKLSSLEG
                                    :* ::.:   :..*:* ** :      :  * .*  **:*** *  :

FL1-18_SPLICE_VARIANT              -MGPSGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPL
FL1-18                             -MGPSGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPL
Drosophila_melanogaster_CG9044     FHMEACKRLQLLNISNNYVEELLDVAKLDALYNLDLSDNCLLEHSQLLPL
imidazoline_receptor_candidate     -LHTKLGNIKTLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSI
                                          :  * : .* :..* .: :*  * :***  * :    :: .:

FL1-18_SPLICE_VARIANT              WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
FL1-18                             WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
Drosophila_melanogaster_CG9044     SALMSLIVLNLQGNPLACNPKHRQATAQYLHKNS--ATVKFVLDFEPLTK
imidazoline_receptor_candidate     GSLPCLEHVSLLNNPLSIIPDYRTKVLAQFGERA----SEVCLDDTVTTE
                                     *  *  : * .***   *.:*  .   :  .:.:    . **    :
```

Figure 8A

```
FL1-18_SPLICE_VARIANT              TDFQTHTS------LGLSPMGPP-LPWPVGSTPETSGGPDLSDSLSSG--
FL1-18                             TDFQTHTS------LGLSPMGPP-LPWPVGSTPETSGGPDLSDSLSSG--
Drosophila_melanogaster_CG9044     AEKALTGSQKWRYISGLSHRSPRSTSMSINSSSASINTSDGSQFSSFGSQ
imidazoline_receptor_candidate     KELDTVEV------LKAIQKAKE--VKSKLSNPEKKGGED-SRLSAAPCI
                                    :                .      .  *.. . .  * *   :

FL1-18_SPLICE_VARIANT              ------G-----VVTQPLLHKVKS-RVR---VRRASISEPS--DTD----
FL1-18                             ------G-----VVTQPLLHKVKS-RVR---VRRASISEPS--DTD----
Drosophila_melanogaster_CG9044     RSVSIRGKNYTLEDNQSMDTSQSSKRISSCKIRTVDIEESSEINTDAASV
imidazoline_receptor_candidate     R----PSSSPPTVAPASASLPQPILSNQGIMFVQEEALASSLSSTDS---
                                          .          .                .   .   .*  .**

FL1-18_SPLICE_VARIANT              --PEPRT--------LNPSPAG-------------------WFVQQHPEL
FL1-18                             --PEPRT--------LNPSPAG-------------------WFVQQHPEL
Drosophila_melanogaster_CG9044     STPNPRSE-------YEEEPDNSHLETKKKIETLRLTYGNEWLKSGNAEL
imidazoline_receptor_candidate     LTPEHQPIAQGCSDSLESIPAG----QAASDDLRDVPGAVGGASPEHAEP
                                     *: :.          :  * .                          :.*

FL1-18_SPLICE_VARIANT              EL-------MSSFRERFG-------RNWLQYRSHLE---PSGNP-----L
FL1-18                             EL-------MSSFRERFG-------RNWLQYRSHLE---PSGNP-----L
Drosophila_melanogaster_CG9044     MLGIE--TPQPTERERNES-----RQLFNEYLGELSGFTEAKNDSEHHNI
imidazoline_receptor_candidate     EVQVVPGSGQIIFLPFTCIGYTATNQDFIQRLSTLIR--QAIERQLPAWI
                                    :                      : : :  . *     : :      :

FL1-18_SPLICE_VARIANT              PATPT-------TSAPSAPPASSQGPDTAPRP-----SPPQE---EARG-
FL1-18                             PATPT-------TSAPSAPPASSQGPDTAPRP-----SPPQE---EARG-
Drosophila_melanogaster_CG9044     SSTPTNNVLLASTFDATITPIKSEANDTSGQTLYETCTEGEETNYESFGN
imidazoline_receptor_candidate     EAANQRE-EGQGEQGEEEDEEEEEEEDVAENRYFEMGPPDVE---EEEGG
                                    ::                   ..:  *.: .      .   *   *  *

FL1-18_SPLICE_VARIANT              ------PQESPQ-KMSEEVRAEP----QEEEE----------------E
FL1-18                             ------PQESPQ-KMSEEVRAEP----QEEEE----------------E
Drosophila_melanogaster_CG9044     NTTELSTEERPPDRHEELLRLYASSSNAQDED----------------P
imidazoline_receptor_candidate     GQGE-EEEEEEEDEEAEEERLALEWALGADEDFLLEHIRILKVLWCFLIH
                                          :*    .  *  *         :*:

FL1-18_SPLICE_VARIANT              KEGKEEKEEGEMV--EQGEEEAGEEEEEEQ-DQKEVEAEL----CRP---
FL1-18                             KEGKEEKEEGEMV--EQGEEEAGEEEEEEQ-DQKEVEAEL----CRP---
Drosophila_melanogaster_CG9044     VSDAESDEETYIVYHEQKPSEVLFLTISSN-FIREKDTLT----ERT---
imidazoline_receptor_candidate     VQGSIRQFAACLVLTDFGIAVFEIPHQESRGSSQHILSSLRFVFCFPHGD
                                    ..   .    :*  :            ...   :.  :         .

FL1-18_SPLICE_VARIANT              LLVCPLEGPEG-----VRGRECFLRVTSA----HLFEVEL------QAAR
FL1-18                             LLVCPLEGPEG-----IRGRECFLRVTSA----HLFEVEL------QAAR
Drosophila_melanogaster_CG9044     KAKWSLKILESC----ERVRSNTLRINFD----TMRKDKQ------ERIY
imidazoline_receptor_candidate     LTEFGFLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMA
                                        :   *       *  .  * :           . .       :

FL1-18_SPLICE_VARIANT              TLERLELQSLEAAEIEPEAQAQRSPRPTGS------DLLPGAPIL-----
FL1-18                             TLERLELQSLEAAEIEPEAQAQRSPRPTGS------DLLPGAPIL-----
Drosophila_melanogaster_CG9044     CVENTLCQELEKKLRDILSQRDLTEMNISIYRCV--NCLTQFTIEQK---
imidazoline_receptor_candidate     MLCSPILYGSHTSLQEFLRQLLTFYKVAGGCQERSQGCFPVYLVYSDKRM
                                    :        .    :   *        .        . :.   :
```

Figure 8B

```
FL1-18_SPLICE_VARIANT             ----SLRFS-----YICPDRQ-------------LRR----YLVLEP-DA
FL1-18                            ----SLRFS-----YICPDRQ-------------LRR----YLVLEP-DA
Drosophila_melanogaster_CG9044    ----SKRYKA--KELRCPDCRSVYVAEVTELSSSLSKPS-GEVAAEPKLS
imidazoline_receptor_candidate    VQTAAGDYSGNIEWASCTLCSAVRRSCCAPSEAVKSAAIPYWLLLTPQHL
                                      :  :.       *.                          :   *

FL1-18_SPLICE_VARIANT             HAAVQELLAVLTPVTNVAREQ-------LGEARDLLLGRFQC-------L
FL1-18                            HAAVQELLAVLTPVTNVAREQ-------LGEARDLLLGRFQC-------L
Drosophila_melanogaster_CG9044    PAMIVEESPVEELAAAINKEES----NSIGKSLASFLFYFDESSFDSNQS
imidazoline_receptor_candidate    NVIKADFNPMPNRGTHNCRNRNSFKLSRVPLSTVLLDPTRSCTQ-PRGAF
                                    .   :  .:    :   ::.       :  :   :    .

FL1-18_SPLICE_VARIANT             RCG--------HEFKPEEPRMGLDSE------EGWRP-LFQKTESPAVCP
FL1-18                            RCG--------HEFKPEEPRMGLDSE------EGWRP-LFQKTGS-----
Drosophila_melanogaster_CG9044    VVGSSNTDRD-MEFRANESDVDIISNPSQSSIEVLDPNYVQSASRKTSEE
imidazoline_receptor_candidate    ADGHVLELLVGYRFVTAIFVLPHEKFHFLRVYNQLRA-SLQDLKTVVIAK
                                    *         .* .    :   .       :   .  .*.

FL1-18_SPLICE_VARIANT             NCGSDHVVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRA
FL1-18                            --GNRESSLWLLLR-LP---------ALSATLLAMVTTLTGPRTAHL-RH
Drosophila_melanogaster_CG9044    RRISQLPHLETIHDEVAK-SKSFIEREFGQLLAEQAQPTTPSTAAPLAPA
imidazoline_receptor_candidate    TPGTGGSPQGSFADGQPAERRASNDQRPQEVPAEALAPAPVEVPAPAPAA
                                     .       .    . . .   :.          .

FL1-18_SPLICE_VARIANT             KNSP-P-QAPSTRDHGSW------------SLSPPPERCGLRSVDHRLRL
FL1-18                            R-------APVTMVVG--------------ASVPP--------------
Drosophila_melanogaster_CG9044    KSAV-PSHVPLTESSSSGSVTDSICTTYEQQATDAPQNLQNSLLTESSNS
imidazoline_receptor_candidate    ASASGPAKTPAPAEASTSALVP--EETPVEAPAPPPAEAPAQYPSEHLIQ
                                    .      ..* .   .                  : .* .       .

FL1-18_SPLICE_VARIANT             FLDVEV-----FSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLL
FL1-18                            -------------------------LSAVAS-------ALWTTDS-----
Drosophila_melanogaster_CG9044    QVSGSD-----AESNSRLKSAEDASLLPFASVFQSTNLLMSSSKKLIESE
imidazoline_receptor_candidate    ATSEENQIPSHLPACPSLRHVASLRGSAIIELFHSSIAEVENEELRHLMW
                                    . .                          ..      .    :   .

FL1-18_SPLICE_VARIANT             KVTGEMREPPASWLQLTLAVPLQDLSGIELGL---AGQSLRLEWAAGAG-
FL1-18                            ---------GSSWMLRCSAMPRRSSS---------AASRCQWHWQATLGS
Drosophila_melanogaster_CG9044    ATVFGTQPYKFNYSDFNDIDHRLKLYFYQRKF---KEDGEHFKWLAKGRI
imidazoline_receptor_candidate    SSVVFYQTPGLEVTACVLLSTKAVYFVLHDGLRRYFSEPLQDFWHQKNTD
                                          .    .                .         .  :  *

FL1-18_SPLICE_VARIANT             -------RCVLLPRDARHCRAFLEELLDVLQSLPPAWRNCVS--ATEEEV
FL1-18                            -------SCALWLCLTAGCTC----------------------------
Drosophila_melanogaster_CG9044    YN-EQTQSLGEGLVVMSNCKCYLMEAFAEPHDDVAKWLRQVVSVAVNRLV
imidazoline_receptor_candidate    YNNSPFHISQCFVLKLSDLQSVNVGLFDQHFRLTGSTPMQVVTCLTRDSY
                                                          .                  .

FL1-18_SPLICE_VARIANT             TPQHRLWPLLEKDSSLEARQFFYLR----------AFLVEGPSTCLVS--
FL1-18                            ------------------------------------------------
Drosophila_melanogaster_CG9044    AIDLLPWKLGLSFTLKDWGGFVLLLHDMLRTESLLNYLQQIPLPEQCK--
imidazoline_receptor_candidate    LTHCFLQHLMVVLSSLERTPSPEPVDKDFYSEFGNKTTGKMENYELIHSS
                                    .              :                    :
```

Figure 8C

```
FL1-18_SPLICE_VARIANT               --LLLTPS------TLFLLDEDAAGSP----------------AEPS---
FL1-18                              --------------------------------------------------
Drosophila_melanogaster_CG9044      --LNHQPS------VTLSHQWETIASEPVKMCSLIPSCQWICDQEKSS--
imidazoline_receptor_candidate      RVKFTYPSEEEIGDLTFTVAQKMAEPEKAPALSILLYVQAFQVGMPPPGC
                                           .             .

FL1-18_SPLICE_VARIANT               -----PPAASGEASEKVPPSGPG----PAVRVREQ---QPLSSLSS----
FL1-18                              --------------------------------------------------
Drosophila_melanogaster_CG9044      ----FEPSLLLITETHLYISGNGKFSWLSDKVQEKP-IQPELSLNQP---
imidazoline_receptor_candidate      CRGPLRPKTLLLTSSEIFLLDEDCVHYPLPEFAKEPPQRDRYRLDDGRRV
                                                 . .              .  ::   .     ..

FL1-18_SPLICE_VARIANT               ------VLLYRSAPEDLRLLFYD----------------EV--------S
FL1-18                              --------------------------------------------------
Drosophila_melanogaster_CG9044      --LSNLVDVERITDQKYAINFID----------------ET--------Q
imidazoline_receptor_candidate      RDLDRVLMGYQTYPQALTLVFDDVQGHDLMGSVTLDHFGEVPGGPARASQ
                                              .   :       :                :         .

FL1-18_SPLICE_VARIANT               RLESFWALRVVCQEQLTALLAWIREPWEELFSIGLRTVIQEALALDR
FL1-18                              -----------------------------------------------
Drosophila_melanogaster_CG9044      NRCEIWKLQFETHANAACCLNVIGKGWEQLFGVPFSLSGT-------
imidazoline_receptor_candidate      GREVQWQVFVPSAESREKLISLLARQWEALCGRELPVELTG------
                                     .         .  :                 :.
```

(* REPRESENTS RESIDUES THAT ARE IDENTICAL IN ALL FOUR PRTEINS; : REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CHARACTER IN 3 OUT OF THE 4 PROTEINS; . REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CAHARACTER IN 2 OUT OF THE 4 PROTEINS).

Figure 8D

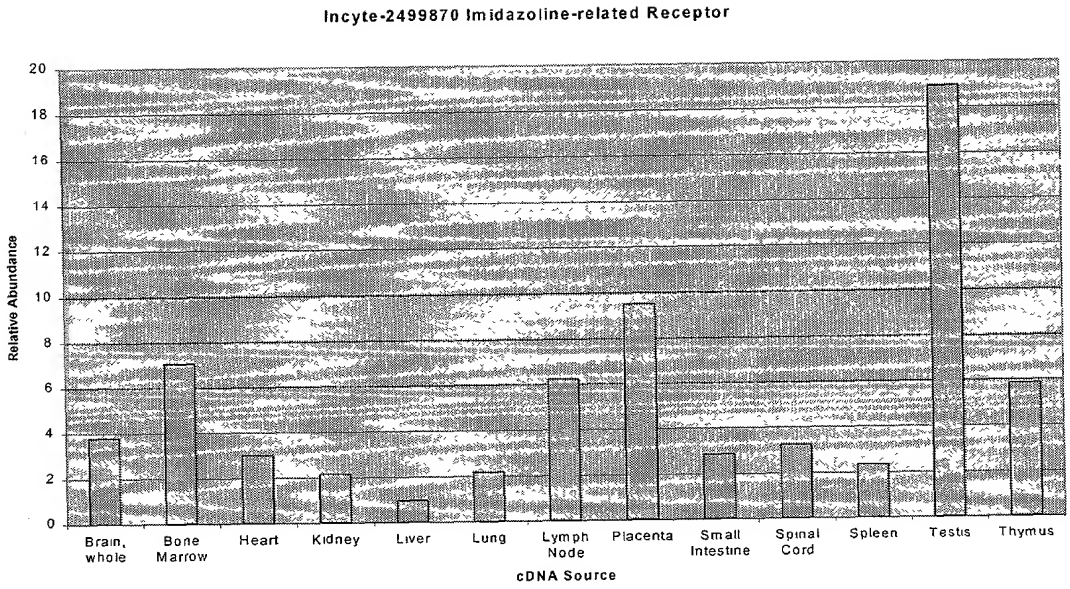
Incyte-2499870 Imidazoline-related Receptor
Relative Abundance
20
18
16
14
12
10
8
6
4
2
0
Brain, whole
Bone Marrow
Heart
Kidney
Liver
Lung
Lymph Node
Placenta
Small Intestine
Spinal Cord
Spleen
Testis
Thymus
cDNA Source

Figure 9.

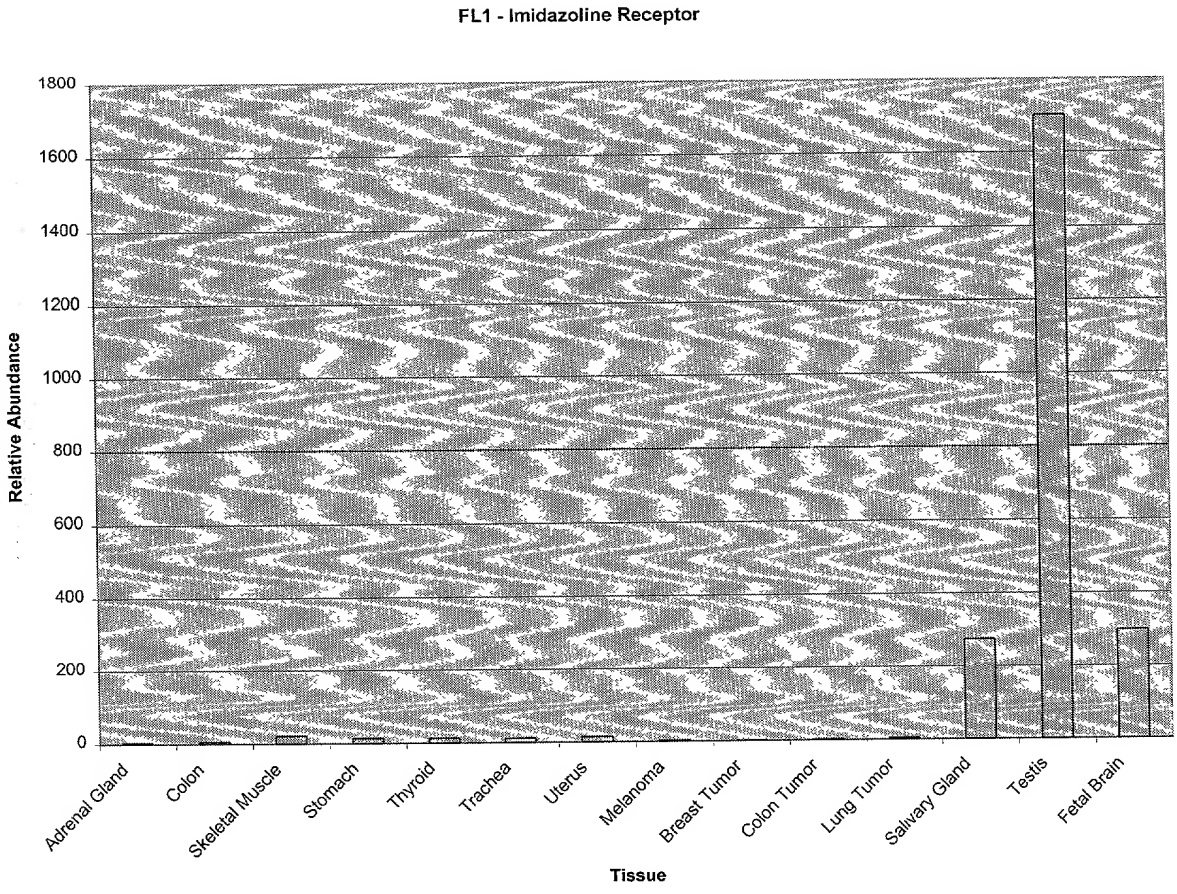

Figure 10.